

RAW SEQUENCE LISTING

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Application Serial Number: 10/519,069
Source: pg 10
Date Processed by STIC: 11/3/05

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PCT

RAW SEQUENCE LISTING

DATE: 11/03/2005

PATENT APPLICATION: US/10/519,069

TIME: 08:23:18

Input Set : A:\Seqlist.txt

Output Set: N:\CRF4\11032005\J519069.raw

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4 <110> APPLICANT: Fritsch Olivier
5     Hohn Barbara
6     Lucht Jan Martin
8 <120> TITLE OF INVENTION: GENE FOR INCREASED SOMATIC RECOMBINATION
11 <130> FILE REFERENCE: 1-32546B/FMI
13 <140> CURRENT APPLICATION NUMBER: 10/519,069
C--> 14 <141> CURRENT FILING DATE: 2004-12-22
16 <150> PRIOR APPLICATION NUMBER: PCT/EP03/006757
17 <151> PRIOR FILING DATE: 2003-06-26
19 <150> PRIOR APPLICATION NUMBER: GB 0214896
20 <151> PRIOR FILING DATE: 2002-06-27
22 <160> NUMBER OF SEQ ID NOS: 30
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 4524
28 <212> TYPE: DNA
29 <213> ORGANISM: Arabidopsis thaliana
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)...(4524)
34 <223> OTHER INFORMATION: Atino80 sequence
36 <400> SEQUENCE: 1
37 atg gat cct tca aga cga cca ccg aag gac tct cct tac gcg aat cta 48
38 Met Asp Pro Ser Arg Arg Pro Pro Lys Asp Ser Pro Tyr Ala Asn Leu
39 1 5 10 15
41 ttc gat ctc gag ccg ttg atg aag ttt aga att ccg aaa cct gaa gat 96
42 Phe Asp Leu Glu Pro Leu Met Lys Phe Arg Ile Pro Lys Pro Glu Asp
43 20 25 30
45 gaa gtt gat tat tat ggg agt agt agc cag gat gaa agt aga agc act 144
46 Glu Val Asp Tyr Tyr Gly Ser Ser Ser Gln Asp Glu Ser Arg Ser Thr
47 35 40 45
49 caa ggt ggg gta gtg gca aac tac agc aat ggg tct aaa tcg aga atg 192
50 Gln Gly Gly Val Val Ala Asn Tyr Ser Asn Gly Ser Lys Ser Arg Met
51 50 55 60
53 aat gcg agc tcc aag aag aga aag cgg tgg aca gaa gct gag gat gca 240
54 Asn Ala Ser Ser Lys Lys Arg Lys Arg Trp Thr Glu Ala Glu Asp Ala
55 65 70 75 80
57 gag gac gat gat gat ctc tac aat caa cat gtt act gag gag cac tac 288
58 Glu Asp Asp Asp Asp Leu Tyr Asn Gln His Val Thr Glu Glu His Tyr
59 85 90 95
61 cga tca atg ctt ggg gag cat gta caa aaa ttc aaa aat agg tcc aag 336
62 Arg Ser Met Leu Gly Glu His Val Gln Lys Phe Lys Asn Arg Ser Lys
63 100 105 110

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65 gag act caa ggg aat cct cct cat ctg atg ggt ttt ccg gtg cta aag 384
66 Glu Thr Gln Gly Asn Pro Pro His Leu Met Gly Phe Pro Val Leu Lys
67      115      120      125
69 agc aat gtg ggc agt tac aga ggt agg aaa cca ggg aat gat tac cat 432
70 Ser Asn Val Gly Ser Tyr Arg Gly Arg Lys Pro Gly Asn Asp Tyr His
71      130      135      140
73 ggg agg ttc tat gac atg gac aac tct cca aat ttt gca gct gat gtg 480
74 Gly Arg Phe Tyr Asp Met Asp Asn Ser Pro Asn Phe Ala Ala Asp Val
75 145      150      155      160
77 acc cca cat agg cga gga agc tac cat gat cgt gat att aca ccc aag 528
78 Thr Pro His Arg Arg Gly Ser Tyr His Asp Arg Asp Ile Thr Pro Lys
79      165      170      175
81 ata gca tat gaa cct tcg tat ttg gac att ggt gat ggt gtc atc tac 576
82 Ile Ala Tyr Glu Pro Ser Tyr Leu Asp Ile Gly Asp Gly Val Ile Tyr
83      180      185      190
85 aaa atc ccc cca agt tat gac aag ctg gtg gca tca tta aac tta ccg 624
86 Lys Ile Pro Pro Ser Tyr Asp Lys Leu Val Ala Ser Leu Asn Leu Pro
87      195      200      205
89 agc ttt tca gac att cat gtg gaa gaa ttt tac ttg aaa gga act ctg 672
90 Ser Phe Ser Asp Ile His Val Glu Glu Phe Tyr Leu Lys Gly Thr Leu
91      210      215      220
93 gat ctg aga tca tta gca gaa ctg atg gca agt gat aaa agg tct gga 720
94 Asp Leu Arg Ser Leu Ala Glu Leu Met Ala Ser Asp Lys Arg Ser Gly
95 225      230      235      240
97 gta aga agc cgt aat gga atg ggt gag cct cga cct caa tat gaa tct 768
98 Val Arg Ser Arg Asn Gly Met Gly Glu Pro Arg Pro Gln Tyr Glu Ser
99      245      250      255
101 ctt caa gct aga atg aag gcc ctg tca cct tca aac tcc acc cca aat 816
102 Leu Gln Ala Arg Met Lys Ala Leu Ser Pro Ser Asn Ser Thr Pro Asn
103      260      265      270
105 ttt agc ctc aag gtg tca gaa gct gca atg aat tct gcc att cca gaa 864
106 Phe Ser Leu Lys Val Ser Glu Ala Ala Met Asn Ser Ala Ile Pro Glu
107      275      280      285
109 gga tct gct gga agt act gca cgg aca att ctg tct gag ggt ggt gtt 912
110 Gly Ser Ala Gly Ser Thr Ala Arg Thr Ile Leu Ser Glu Gly Gly Val
111      290      295      300
113 tta cag gtc cat tac gtg aag att ctg gag aag ggg gat aca tac gag 960
114 Leu Gln Val His Tyr Val Lys Ile Leu Glu Lys Gly Asp Thr Tyr Glu
115 305      310      315      320
117 att gtt aaa cga agt cta ccg aag aag ctg aaa gca aag aat gat cct 1008
118 Ile Val Lys Arg Ser Leu Pro Lys Lys Leu Lys Ala Lys Asn Asp Pro
119      325      330      335
121 gca gtc att gag aaa aca gaa agg gat aaa att aga aaa gcc tgg atc 1056
122 Ala Val Ile Glu Lys Thr Glu Arg Asp Lys Ile Arg Lys Ala Trp Ile
123      340      345      350
125 aat att gtc aga aga gat ata gca aaa cac cat aga att ttc act act 1104
126 Asn Ile Val Arg Arg Asp Ile Ala Lys His His Arg Ile Phe Thr Thr
127      355      360      365
129 ttt cat cgt aaa cta tca att gat gcc aag agg ttt gca gat ggt tgc 1152

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130	Phe	His	Arg	Lys	Leu	Ser	Ile	Asp	Ala	Lys	Arg	Phe	Ala	Asp	Gly	Cys	
131		370					375					380					
133	caa	aga	gag	gtg	aga	atg	aag	gtg	ggt	aga	tca	tac	aaa	atc	cca	aga	1200
134	Gln	Arg	Glu	Val	Arg	Met	Lys	Val	Gly	Arg	Ser	Tyr	Lys	Ile	Pro	Arg	
135	385					390					395					400	
137	act	gca	cca	att	cgc	act	agg	aag	ata	tcc	aga	gac	atg	ctg	cta	ttc	1248
138	Thr	Ala	Pro	Ile	Arg	Thr	Arg	Lys	Ile	Ser	Arg	Asp	Met	Leu	Leu	Phe	
139				405					410					415			
141	tgg	aag	cga	tat	gac	aag	cag	atg	gca	gaa	gag	agg	aaa	aag	caa	gaa	1296
142	Trp	Lys	Arg	Tyr	Asp	Lys	Gln	Met	Ala	Glu	Glu	Arg	Lys	Lys	Gln	Glu	
143			420					425					430				
145	aag	gaa	gct	gca	gag	gct	ttt	aaa	cgt	gaa	cag	gag	cag	cga	gag	tca	1344
146	Lys	Glu	Ala	Ala	Glu	Ala	Phe	Lys	Arg	Glu	Gln	Glu	Gln	Arg	Glu	Ser	
147			435					440					445				
149	aaa	agg	cag	caa	caa	agg	ctc	aat	ttc	ctt	att	aaa	cag	act	gag	ctt	1392
150	Lys	Arg	Gln	Gln	Gln	Arg	Leu	Asn	Phe	Leu	Ile	Lys	Gln	Thr	Glu	Leu	
151		450					455					460					
153	tac	agt	cac	ttc	atg	caa	aac	aag	acc	gat	tgc	aat	cct	tcc	gaa	gcc	1440
154	Tyr	Ser	His	Phe	Met	Gln	Asn	Lys	Thr	Asp	Ser	Asn	Pro	Ser	Glu	Ala	
155	465				470					475					480		
157	tta	cca	ata	ggt	gat	gaa	aat	ccg	att	gac	gaa	gtg	ctc	cca	gaa	act	1488
158	Leu	Pro	Ile	Gly	Asp	Glu	Asn	Pro	Ile	Asp	Glu	Val	Leu	Pro	Glu	Thr	
159				485					490						495		
161	tca	gcg	gca	gaa	cct	tct	gag	gta	gag	gat	cct	gaa	gag	gct	gaa	ctg	1536
162	Ser	Ala	Ala	Glu	Pro	Ser	Glu	Val	Glu	Asp	Pro	Glu	Glu	Ala	Glu	Leu	
163			500					505					510				
165	aag	gaa	aag	gtc	ttg	aga	gct	gcc	caa	gat	gcg	gtg	tct	aag	cag	aag	1584
166	Lys	Glu	Lys	Val	Leu	Arg	Ala	Ala	Gln	Asp	Ala	Val	Ser	Lys	Gln	Lys	
167			515					520					525				
169	caa	ata	aca	gat	gca	ttt	gac	act	gaa	tat	atg	aag	cta	cgc	caa	act	1632
170	Gln	Ile	Thr	Asp	Ala	Phe	Asp	Thr	Glu	Tyr	Met	Lys	Leu	Arg	Gln	Thr	
171		530					535					540					
173	tct	gaa	atg	gaa	ggt	cct	tta	aat	gat	ata	tca	gtt	tct	ggc	tgc	agc	1680
174	Ser	Glu	Met	Glu	Gly	Pro	Leu	Asn	Asp	Ile	Ser	Val	Ser	Gly	Ser	Ser	
175	545				550					555					560		
177	aat	ata	gat	ttg	cat	aac	cca	tct	aca	atg	cct	gtt	aca	tca	aca	gtt	1728
178	Asn	Ile	Asp	Leu	His	Asn	Pro	Ser	Thr	Met	Pro	Val	Thr	Ser	Thr	Val	
179				565					570						575		
181	cag	act	cca	gag	tta	ttt	aaa	gga	acc	ctt	aaa	gaa	tac	caa	atg	aaa	1776
182	Gln	Thr	Pro	Glu	Leu	Phe	Lys	Gly	Thr	Leu	Lys	Glu	Tyr	Gln	Met	Lys	
183			580					585					590				
185	ggc	ctt	cag	tgg	cta	gtc	aat	tgt	tat	gag	cag	ggt	ttg	aat	ggc	ata	1824
186	Gly	Leu	Gln	Trp	Leu	Val	Asn	Cys	Tyr	Glu	Gln	Gly	Leu	Asn	Gly	Ile	
187			595				600					605					
189	ctt	gct	gat	gaa	atg	ggc	ttg	ggt	aag	act	att	caa	gct	atg	gcg	ttc	1872
190	Leu	Ala	Asp	Glu	Met	Gly	Leu	Gly	Lys	Thr	Ile	Gln	Ala	Met	Ala	Phe	
191		610					615					620					
193	ttg	gca	cat	ttg	gct	gag	gaa	aag	aac	att	tgg	ggt	cca	ttt	ctt	gtt	1920
194	Leu	Ala	His	Leu	Ala	Glu	Glu	Lys	Asn	Ile	Trp	Gly	Pro	Phe	Leu	Val	

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195	625		630		635		640	
197	ggt	gcc	cct	gcc	tct	ggt	ctt	aac aat tgg gct gat gaa atc agt cgt 1968
198	Val	Ala	Pro	Ala	Ser	Val	Leu	Asn Asn Trp Ala Asp Glu Ile Ser Arg
199				645				650 655
201	ttc	tgt	cct	gac	ttg	aaa	act	ctt cca tat tgg gga gga tta caa gaa 2016
202	Phe	Cys	Pro	Asp	Leu	Lys	Thr	Leu Pro Tyr Trp Gly Gly Leu Gln Glu
203				660				665 670
205	cga	aca	att	tta	aga	aag	aat	atc aat ccc aag cgt atg tac cga agg 2064
206	Arg	Thr	Ile	Leu	Arg	Lys	Asn	Ile Asn Pro Lys Arg Met Tyr Arg Arg
207				675				680 685
209	gat	gct	ggc	ttt	cat	att	ttg	att act agc tat cag cta tta gtc act 2112
210	Asp	Ala	Gly	Phe	His	Ile	Leu	Ile Thr Ser Tyr Gln Leu Leu Val Thr
211				690				695 700
213	gat	gaa	aag	tat	ttt	cgc	cgg	gtg aag tgg caa tat atg gtg cta gat 2160
214	Asp	Glu	Lys	Tyr	Phe	Arg	Arg	Val Lys Trp Gln Tyr Met Val Leu Asp
215	705							710 715 720
217	gag	gcc	caa	gca	atc	aag	agt	tcc tcc agt ata aga tgg aaa acc ctt 2208
218	Glu	Ala	Gln	Ala	Ile	Lys	Ser	Ser Ser Ser Ile Arg Trp Lys Thr Leu
219				725				730 735
221	ctt	agt	ttt	aac	tgt	cgg	aac	cga ttg ctt ctg act ggt act cca att 2256
222	Leu	Ser	Phe	Asn	Cys	Arg	Asn	Arg Leu Leu Leu Thr Gly Thr Pro Ile
223				740				745 750
225	cag	aac	aac	atg	gca	gag	tta	tgg gcc ctg ctg cat ttc atc atg cca 2304
226	Gln	Asn	Asn	Met	Ala	Glu	Leu	Trp Ala Leu Leu His Phe Ile Met Pro
227				755				760 765
229	atg	ttg	ttt	gac	aac	cat	gat	caa ttt aat gaa tgg ttc tca aaa gga 2352
230	Met	Leu	Phe	Asp	Asn	His	Asp	Gln Phe Asn Glu Trp Phe Ser Lys Gly
231				770				775 780
233	att	gag	aat	cat	gct	gaa	cac	gga ggc act tta aat gag cac cag ctt 2400
234	Ile	Glu	Asn	His	Ala	Glu	His	Gly Gly Thr Leu Asn Glu His Gln Leu
235	785							790 795 800
237	aac	aga	ctg	cat	gcg	atc	ttg	aaa ccg ttc atg ctt cga cgg gta aaa 2448
238	Asn	Arg	Leu	His	Ala	Ile	Leu	Lys Pro Phe Met Leu Arg Arg Val Lys
239				805				810 815
241	aag	gat	gtg	ggt	tct	gag	cta	act aca aag acg gaa gtt aca gta cac 2496
242	Lys	Asp	Val	Val	Ser	Glu	Leu	Thr Thr Lys Thr Glu Val Thr Val His
243				820				825 830
245	tgc	aag	ctc	agt	tct	cga	caa	caa gct ttt tat cag gct att aag aac 2544
246	Cys	Lys	Leu	Ser	Ser	Arg	Gln	Gln Ala Phe Tyr Gln Ala Ile Lys Asn
247				835				840 845
249	aaa	att	tct	ctg	gct	gag	ttg	ttt gat agc aac cgc gga caa ttt act 2592
250	Lys	Ile	Ser	Leu	Ala	Glu	Leu	Phe Asp Ser Asn Arg Gly Gln Phe Thr
251				850				855 860
253	gat	aag	aaa	gta	ttg	aat	tta	atg aat att gtc att caa cta agg aag 2640
254	Asp	Lys	Lys	Val	Leu	Asn	Leu	Met Asn Ile Val Ile Gln Leu Arg Lys
255	865							870 875 880
257	ggt	tgc	aac	cat	cca	gag	ttg	ttc gaa agg aat gaa ggg agc tcg tat 2688
258	Val	Cys	Asn	His	Pro	Glu	Leu	Phe Glu Arg Asn Glu Gly Ser Ser Tyr
259				885				890 895

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261 ctc tac ttt gga gtg act tcc aat tct ctt ttg ccc cat ccc ttt ggt 2736
262 Leu Tyr Phe Gly Val Thr Ser Asn Ser Leu Leu Pro His Pro Phe Gly
263          900          905          910
265 gag cta gag gat gta cat tat tct ggt ggt caa aat ccg ata ata tac 2784
266 Glu Leu Glu Asp Val His Tyr Ser Gly Gly Gln Asn Pro Ile Ile Tyr
267          915          920          925
269 aag ata cct aag cta cta cac caa gag gtg ctc caa aat tct gaa aca 2832
270 Lys Ile Pro Lys Leu Leu His Gln Glu Val Leu Gln Asn Ser Glu Thr
271          930          935          940
273 ttt tgt tct tct gtc ggg cgt ggc atc tca aga gaa tct ttt ctg aag 2880
274 Phe Cys Ser Ser Val Gly Arg Gly Ile Ser Arg Glu Ser Phe Leu Lys
275 945          950          955          960
277 cat ttt aat ata tat tca cct gag tat att ctt aag tca ata ttc cca 2928
278 His Phe Asn Ile Tyr Ser Pro Glu Tyr Ile Leu Lys Ser Ile Phe Pro
279          965          970          975
281 tct gat agt ggg gta gat caa gtg gtt agt gga agt gga gca ttt ggc 2976
282 Ser Asp Ser Gly Val Asp Gln Val Val Ser Gly Ser Gly Ala Phe Gly
283          980          985          990
285 ttt tca cgc ttg atg gat cta tca cca tca gaa gtt gga tat ctg gct 3024
286 Phe Ser Arg Leu Met Asp Leu Ser Pro Ser Glu Val Gly Tyr Leu Ala
287          995          1000          1005
289 ctg tgt tct gtt gca gaa agg cta tta ttt tct ata ctg agg tgg gag 3072
290 Leu Cys Ser Val Ala Glu Arg Leu Leu Phe Ser Ile Leu Arg Trp Glu
291          1010          1015          1020
293 cgg caa ttt ttg gat gaa tta gtt aac tct ctt atg gag tcc aag gat 3120
294 Arg Gln Phe Leu Asp Glu Leu Val Asn Ser Leu Met Glu Ser Lys Asp
295 1025          1030          1035          1040
297 ggt gat ctt agt gac aat aac atc gag aga gtt aaa acc aaa gct gtc 3168
298 Gly Asp Leu Ser Asp Asn Asn Ile Glu Arg Val Lys Thr Lys Ala Val
299          1045          1050          1055
301 aca aga atg ttg ctg atg cca tca aaa gtt gaa acg aat ttt cag aaa 3216
302 Thr Arg Met Leu Leu Met Pro Ser Lys Val Glu Thr Asn Phe Gln Lys
303          1060          1065          1070
305 agg aga cta agc aca ggg cct acc cgt cct tca ttt gaa gcg cta gtg 3264
306 Arg Arg Leu Ser Thr Gly Pro Thr Arg Pro Ser Phe Glu Ala Leu Val
307          1075          1080          1085
309 atc tct cat cag gat agg ttt ctt tca agt atc aaa ctc ctg cat tct 3312
310 Ile Ser His Gln Asp Arg Phe Leu Ser Ser Ile Lys Leu Leu His Ser
311          1090          1095          1100
313 gca tat act tat atc cca aaa gcc aga gct cca cct gta agc att cat 3360
314 Ala Tyr Thr Tyr Ile Pro Lys Ala Arg Ala Pro Pro Val Ser Ile His
315 1105          1110          1115          1120
317 tgc tcg gac aga aat tcg gca tac aga gtt aca gaa gaa tta cat caa 3408
318 Cys Ser Asp Arg Asn Ser Ala Tyr Arg Val Thr Glu Glu Leu His Gln
319          1125          1130          1135
321 cca tgg ctt aag aga cta tta atc ggt ttt gca cga acg tca gaa gct 3456
322 Pro Trp Leu Lys Arg Leu Leu Ile Gly Phe Ala Arg Thr Ser Glu Ala
323          1140          1145          1150
325 aat gga ccc agg aag cct aac agc ttt cca cat cct tta atc caa gaa 3504

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VERIFICATION SUMMARY

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date